

AMENDMENTS TO THE SPECIFICATION:

Please replace the paragraph that bridges pages 28-29 beginning at page 28, line 15, with the following paragraph:

The determination of percent identity between two sequences can also be accomplished using a mathematical algorithm. A preferred, non-limiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul, 1990, Proc. Natl. Acad. Sci. USA 87:2264-2268, modified as in Karlin and Altschul, 1993, Proc. Natl. Acad. Sci. USA 90:5873-5877. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul, et al., 1990, J. Mol. Biol. 215:403-410. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to a nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to a protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al., 1997, Nucleic Acids Res. 25:3389-3402. Alternatively, PSI-Blast can be used to perform an iterated search which detects distant relationships between molecules (Altschul et al., 1997, *supra*). When utilizing BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the respective programs (*e.g.*, XBLAST and NBLAST) can be used (see <http://www.ncbi.nlm.nih.gov> the National Center for Biotechnology Information/ NCBI website). Another preferred, non-limiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul, 1990, *Proc. Natl. Acad. Sci. USA* 87:2264, modified as in Karlin and Altschul, 1993, *Proc. Natl. Acad. Sci. USA* 90:5873. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul, et al., 1990, *J. Mol. Biol.* 215:403. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to a nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to a protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul, et al., 1997, *Nucleic Acids*

Res. 25:3389. Alternatively, PSI-Blast can be used to perform an iterated search which detects distant relationships between molecules (Altschul, et al., 1997, *supra*). When utilizing BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the respective programs (*e.g.*, XBLAST and NBLAST) can be used (see <http://www.ncbi.nlm.nih.gov> the National Center for Biotechnology Information/ NCBI website). Another preferred, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller, 1988, *CABIOS* 4:11. Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used.

Please replace the paragraph that begins at page 80, line 4, with the following paragraph:

DNA database searches and analysis of protein motifs. ESTs (expressed sequence tags) with homology to FBP genes were identified using BLAST, PSI-BLAST (<http://www.ncbi.nlm.nih.gov> see the National Center for Biotechnology Information/ NCBI website) and TGI Sequence Search (http://www.tigr.org/egi-bin/BlastSearch/blast_tgi.cgi see The Institute for Genomic Research/TIGR website). ESTs that overlapped more than 95 % in at least 100 bps were assembled into novel contiguous ORFs using Sequencher 3.0. Protein domains were identified with ProfileScan Server (http://www.isrec.isb-sib.ch/software/PFSCAN_form.html available at the Swiss Institute for Experimental Cancer Research/ISREC website), BLOCKS Searcher (http://www.blocks.fhcrc.org/blocks_search.html see the Blocks www server at the Fred Hutchinson Cancer Research Center/FHCRC website) and IMB Jena (<http://genome.imb-jena.de/egi-bin/GDEWWW/menu.cgi> available at the Institute for Molecular Biotechnology/IMB website).